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OM protein - protein search, using sw model

Run on: June 23, 2003, 08:28:51 ; Search time 20.5204 Seconds

(without alignments)
371.904 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964
Sequence: 1 MLOWAGCCGNEYPDSLHA.....CKSLPALATIEKISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	TR17_HUMAN	002223 homo sapien
2	572	59.3	185	TR17_MOUSE	088472 mus musculu
3	116.5	12.1	175	TI13_MOUSE	0948d0 mus musculu
4	94	9.8	323	TNR6_BOVIN	P51667 bos taurus
5	93	9.6	184	TI13_HUMAN	0964j3 homo sapien
6	86.5	9.0	867	PROM_MOUSE	054930 mus musculu
7	82	8.5	1009	PAK2_MOUSE	0949p9 m proteini t
8	82	8.5	1009	PAK2_RAT	P70600 rattus norv
9	79.5	8.2	1009	PAK2_HUMAN	Q14289 h protein t
10	78.5	8.1	293	TI13_HUMAN	014836 homo sapien
11	78.5	8.1	343	YD57_MERTIA	058752 methanococc
12	77	8.0	249	TI13_MOUSE	09e435 mus musculu
13	75.5	7.8	638	YCSB_SCHPO	074910 schizosach
14	75	7.8	849	SRK6_BRAOL	009092 brassica ol
15	74.5	7.7	384	ERD1_KULIA	P41771 kluyveromyc
16	72.5	7.5	1013	PRML_DROME	P82295 drosophila
17	71.5	7.4	105	Y078_NPVOP	010331 oxygia pseu
18	71.5	7.4	627	Y017_RICPR	092ec6 rickettsia
19	71	7.4	227	COMB_THEMA	09wq44 thermotoga
20	70.5	7.3	188	Y101_UREPA	09p443 ureaplasma
21	70.5	7.3	1203	MGR5_RAT	P31424 rattus norv
22	70.5	7.3	1877	PCK5_MOUSE	004592 mus musculu
23	70.5	7.3	2715	G156_PAPRP	P13837 parametium
24	70	7.3	654	HS70_TRIRU	093866 trichophyto
25	69.5	7.2	573	TLPC_BACSU	P39209 bacillus su
26	69.5	7.2	1212	MGR5_HUMAN	P41594 homo sapien
27	69.5	7.2	5376	ZAN_MOUSE	088799 mus musculu
28	69	7.2	324	GCI_MOUSE	P01868 mus musculu
29	69	7.2	352	C5AE_RAT	P97520 rattus norv
30	69	7.2	379	PANE_YEAST	P38787 saccharomyc
31	69	7.2	393	GCIH_MOUSE	P01869 mus musculu
32	69	7.2	416	R23B_MOUSE	P54728 mus musculu
33	68.5	7.1	321	OSV1_HUMAN	09ugf6 homo sapien

34	68.5	7.1	328	1	Y679_CHILMU	Q9pj27 chlamydia m
35	68.5	7.1	409	1	R23B_HUMAN	P54727 homo sapien
36	68.5	7.1	575	1	C622_CUCMA	O05046 cucurbita m
37	68.5	7.1	576	1	CH62_MAIZE	O43298 zea mays (m
38	68.5	7.1	577	1	CH61_MAIZE	P29185 zea mays (m
39	68	7.1	590	1	ACCD_PEA	P18823 pisum sativ
40	68	7.1	1140	1	RA18_SCHPO	P53692 schizosach
41	68	7.1	1203	1	XCPE_XENLA	P50533 xenopus lae
42	68	7.1	2158	1	MY9B_HUMAN	O13459 homo sapien
43	68	7.1	3386	1	POLG_DEN4	P09866 d genome po
44	67.5	7.0	178	1	LACB_BOVIN	P02754 bos taurus
45	67.5	7.0	245	1	YH77_ARCFU	O28497 archaeglob

ALIGNMENTS

RESULT 1	ID	TR17_HUMAN	STANDARD;	PRT;	184 AA.
AC	002223;				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).				
GN	TNFRSF17 OR BCMA OR BCM.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
OX	[1]				
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.				
RC	TISSUE-Peripheral blood leukocytes, and lymph node.				
RX	MEDLINE=93010984; PubMed=1396583;				
RA	Laabi Y., Gras M.P., Cardonnel F., Brouet J.C., Berger R.,				
RA	Larsen C.J., Tsapis A.;				
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";				
RT	EMBO J. 11:3897-3904(1992).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=94218235; PubMed=8165126;				
RX	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RA	"The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";				
RT	Nucleic Acids Res. 22:1147-1154(1994).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=9425270; PubMed=10492829;				
RX	Loftus B.J., Kim U.-J., Sneedon V.P., Kalush F., Brandon R.,				
RA	Fuhrman J., Mason T., Crosby M.L., Barnstead M., Cronin L.,				
RA	Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,				
RA	Bichter E.E., Harris P.C., Venter J.C., Adams M.D.;				
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";				
RT	Genomics 60:295-308(1999).				
RL	[4]				
RN	SEQUENCE FROM N.A., AND VARIANT THR-153.				
RP	MEDLINE=21419161; PubMed=11528522;				
RX	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;				
RT	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";				
RT	Genes Immun. 2:276-279(2001).				
RL	[5]				
RN	FUNCTION.				
RP	MEDLINE=2036316; PubMed=10903733;				
RX	Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,				
RA	Inoue J., Devergne O., Tsapis A.;				
RT	"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38				

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1332-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Litteu A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.;
 RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 auto-immune disease.";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theil L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 DR EMBL; 214954; CAA78679.1; -;
 DR EMBL; 229575; CAA82691.1; -;
 DR EMBL; 229574; CAA82690.1; -;
 DR EMBL; U95742; AAB67251.1; -;
 DR EMBL; AB052772; BAB60895.1; -;
 DR PIR; S31208; S31208.
 DR PIR; S31209; S31209.
 DR Gene; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -;
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KW TRANSMEM 1 54
 KW SIGNAL-ANCHOR (POTENTIAL).
 KW TRANSMEM 55 77
 KW CYTOPLASMIC (POTENTIAL).
 KW POTENTIAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 KW TNFR-CYS.
 KW BREAKPOINT FOR TRANSLOCATION TO FORM
 KW INTERLEUKIN 2/BCM ONCOGENE.
 KW DISUPEID 8 21
 KW DISUPEID 24 37
 KW DISUPEID 26 41
 KW VARIANT 153 153
 KW A -> T.
 KW /FTID=VAR_012234.
 KW SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1,3e-83;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWMAGQCSQNEYFDSLLHACIPQQLRCCSNTPPTLCQRYCNASVTSVKGTAIWLTC 60
 DB 1 MWMAGQCSQNEYFDSLLHACIPQQLRCCSNTPPTLCQRYCNASVTSVKGTAIWLTC 60
 QY 61 GSIILISLAVFLMFLKRISEPKDEPKNGSLGMANDLKSRTGDEIILPRGE 120
 DB 61 GSIILISLAVFLMFLKRISEPKDEPKNGSLGMANDLKSRTGDEIILPRGE 120
 QY 121 YVSECTCEDCKSKPKYSDHCFPLPAMEGATLVTTKNDYKSLPALATIEIKS 180
 DB 121 YVSECTCEDCKSKPKYSDHCFPLPAMEGATLVTTKNDYKSLPALATIEIKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 2
 ID TR17 MOUSE STANDARD; PRI; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
 RP STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglu A.,
 RA Le Conlat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RL of the tumor necrosis factor receptor superfamily.";
 RN Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=C57BL/6J; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gasteierland T., Gissi C., King B., Koshida H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Queckenbush J.,
 RA Schriml L.W., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereaux P.,
 RA Nordone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlschki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by

CC similarity).

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are

CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and

CC heart, and at lower levels in kidney and lung.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

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CC -----

DR EMBL: AF061505; AAC23799.1; -

DR EMBL: AK020247; BAB32038.1; -

DR MGD: MGI:1343050; Tnfrsf17.

DR Receptor; Immune response; Signal-anchor; Transmembrane;

DR Alternative splicing.

DR DOMAIN 1 49 EXTRACELLULAR (POTENTIAL)

DR TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

DR DOMAIN 71 185 (POTENTIAL)

DR REPEAT 4 36 CYTOPLASMIC (POTENTIAL).

DR DISULFID 5 18 TNFR-CYS.

DR DISULFID 21 32 BY SIMILARITY.

DR DISULFID 25 36 BY SIMILARITY.

DR VARSPLIC 87 91 MISSING (IN ISOFORM 2).

DR SEQUENCE 185 AA; 20442 MW; 8806352BAFD26A8E CRC64;

Query Match 59.3%; Score 572; DB 1; Length 185;

Best Local Similarity 62.6%; Pred. No. 8.7e-47;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGQSQNEFDPSLLHACIPCOLRCSNTPPTQCRYYCNASYNSYKGNALMTWCLGIS 63

DB 1 MAQCFHSEYFDPSLLHACKRCHLRGNN--PPATTCQYCDPSTSVSKGYTVMFLIGLT 58

QY 64 LIISLAVFLMLFKRISEPIKDEPKR---TGSGLLGMANIDFKSTGTGEBIILPRGL 119

DB 59 IVLISLALFTISFLKRMPEAKDEPQSGOLDGSHQDKADTELRIKAGDRIFFPRSL 118

QY 120 EYTVECTCECDCKSPKXVDSDHCFPLPMERGAATLVTTKTNDCYK-SLPAAL-SATFI 177

DB 119 EYTVECTCECDCKSPKXVDSDHCFPLPMERGAATLVTTKTDYKSSVPTALOSVWGM 178

178 EKSIASR 184

179 EKPTRTR 185

Db

RESULT 3

T13C MOUSE STANDARD; PRT; 175 AA.

AC 09DSD0;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 13C (B cell-

DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor

DE 3) (B-cell maturation defect).

GN TNFRSF13C OR BAFFR OR BCMD OR BR3.

OS Mus musculus (Mouse); Chordata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID:10090;

RP [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN-BALB/c; TISSUE=B-cell lymphoma;

RX MEDLINE=21442025; PubMed=11509592;

RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,

RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,

RA Strach K., Zafar M., Benjamin C.D., Teichp J., Browning J.L.,

RA Ambrose C.;

RT "BAFF-R, a newly identified TNF receptor that specifically interacts

RT with BAFF.";

RL Science 293:2108-2111 (2001).

RP [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.

RC STRAIN=A/J;

RX MEDLINE=21475520; PubMed=11591325;

RX Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,

RA Canoro M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that

RT is mutated in a mouse strain with severe B cell deficiency.";

RL Curr. Biol. 11:1547-1552 (2001).

RP [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=21085660; PubMed=11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojopori T., Bono H., Kasukawa T., Saito K.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Hono H., Baldarelli R., Barsh G.,

RA Blake J., Botfeill D., Boujunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Saeki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,

RA Hayashizaki Y.;

RL "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690 (2001).

RP [4]

RP FUNCTION.

RX MEDLINE=21614654; PubMed=11747827;

RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,

RA Hilbert D.M., Hayes C.E., Cancro M.P.;

RT "Competition for Blys-mediated signaling through Bcmd/BR3 regulates

RT peripheral B lymphocyte numbers.";

RL Curr. Biol. 11:1986-1989 (2001).

CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TNLI/BAFF/Blys.

CC Promotes the survival of mature B-cells and the B-cell response.

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable)

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are

CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;

CC detected at lower levels in lung and thymus.

CC -1- DISEASE: Defects in TNFSF13C are a cause of severe B-cell

CC deficiency. B-cell deficient strain A/WShu has a 4.7 kb insertion

CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA

CC is not detectable. B-cell lymphoproliferosis is normal, but the life

CC span of peripheral B-cells is much reduced.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

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CC -----

DR EMBL: AF373847; AAK91827.1; -

DR EMBL: AK008142; BAB25490.1; -

DR MGD: MGI:1919299; Tnfrsf13c.

DR Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;

Alternative splicing.
 KM DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT 93 (POTENTIAL).
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 36 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 133 143 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 175 AA; 18798 MW; 286C7C1A02PB87EF CRC64;
 Query Match 12.1%; Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.0051;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
 QY 7 QCSQNEYPFSLHACIPCOL-----RCSNTPLTCQRYCNASTNSYK--GYNAIL 56
 DB 21 QCNQTECFDPLVNCVSCCELFTPTDGTHTSSLEFGTALPQEGSALRPVALVGPALL 80
 DB 57 WTCLGLSLI--ISLAFVLMFLRKIS---SEPLKDFKNTSGGLGMANIDEXRTGD 111
 DB 81 GLILALTLVGLVSLVSMRMRQQLTASPTDSGVQGE-----SLENVFPSSSET-- 129
 QY 112 EILIPRGLEYTVECTCECDIKSKPKVSDHCFPLPAMEBGATILVTKY 161
 DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVATHELSTELVTKT 170
 Db
 RESULT 4
 ID TNFR6 BOVIN STANDARD; PRT; 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.
 OC NCB1_Taxid=9913;
 RX (1)
 RP SEQUENCE FROM N.A.
 NY MEDLINE=96226401; PubMed=8634151;
 Yoo J., Stone R.T., Beattie C.W.;
 "Cloning and characterization of the bovine Fas.",
 DNA Cell Biol. 15:227-234(1996).
 DB
 DB 1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC
 CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC 1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC
 CC 1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC
 CC 1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC

DR EMBL; U34794; AAC48546.1; -.
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR Pfam; PF00531; death; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
 FT 17 323 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 17 170 POTENTIAL.
 FT TRANSMEM 171 188 CYTOPLASMIC (POTENTIAL).
 FT 189 323 TNFR-CYS 1.
 FT REPEAT 45 80 TNFR-CYS 2.
 FT REPEAT 81 124 TNFR-CYS 3.
 FT REPEAT 125 163 DEATH.
 FT DOMAIN 238 306 BY SIMILARITY.
 FT DISULFID 45 56 BY SIMILARITY.
 FT DISULFID 57 70 BY SIMILARITY.
 FT DISULFID 60 79 BY SIMILARITY.
 FT DISULFID 82 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 140 BY SIMILARITY.
 FT DISULFID 143 154 BY SIMILARITY.
 FT DISULFID 146 162 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 323 AA; 36445 MW; 4D88A90B9E1F4892 CRC64;
 Query Match 9.8%; Score 94; DB 1; Length 323;
 Best Local Similarity 22.1%; Pred. No. 0.13;
 Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;
 QY 8 CSQ-NEYRPSDLHA--CIPCOL-----RCSN-----T 32
 DB 82 CSEGEYTDKSHSHKXCTRCSCDEHGLEVBQNTTRNTKCKKSNFPCNSPCEHCN 141
 QY 33 PPLTCQ----RYCNASTNSYKTVNA--ILWTCGLSLISLAVFVLMFLRKISSEPL 85
 DB 142 PCTTCEHGLEIKCTPTSNWTKKSGSHANSJMAL-----LILIPVLIIYKVVSRENNK 197
 QY 86 KDFKNTSGG-----LGMANIDL-----EKSTGD--EILIPRGLEYTVECTCED 130
 DB 198 KNDYCNSAASNDGRLNLTVDLQKYPISIAEQWRITEVEKEFYKNGM-----BEAKTID 253
 DB 254 IWH-----DNVA---ETAEQKVQLRWYVSHGKKNVCTLTSLSPALA 295
 QY 131 CIKSKPKVSDHCFPLPAMEBGATILV-----TKTNDYC---KSLPAALS 173
 DB
 DB 1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC
 CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC 1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC
 CC 1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC
 CC 1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC

RTISUB-B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Strauch K., Zafar M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RT "BAF-R", a newly identified TNF receptor that specifically interacts
 RT with BAF-R";
 RL Science 293:2108-2111 (2001).

RP [2]

FUNCTION.

RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hau B., Harless S.M.,
 RA Canero M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency.";
 RL Curr. Biol. 11:1547-1552 (2001).

CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
 CC in resting B-cells. Detected at lower levels in activated B-cells,
 CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC

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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF373846; AAK91826.1; -
 CC Genew; HGNC:17755; TNFRSF13C.

DR MIM: 606269; -
 DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.

DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.

FT DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT TRANSMEM 79 99 (POTENTIAL).

FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 18 35 TNFR-CYS (PARTIAL).
 FT DISULFID 19 32 BY SIMILARITY.

FT DISULFID 24 35 BY SIMILARITY.
 FT VARSPLIC 143 143 P -> PA (IN ISOGORM 2).
 SQ SEQUENCE 184 AA, 18863 MW, F2BFB9809A27138 CR664;

Query Match 9.6%; Score 93; DB 1; Length 184;
 Best Local Similarity 26.5%; Pred. No. 0.088;
 Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

QY 8 CSQNYEFDLSHACIPCOL-----RCSSNTP--PLTCQRYCNASTYNSVKGNAL 56
 Db 19 CVPACSCFDLVHCAACGLRTPPKAGASSPAPPTALQPOESVAGAGEALPLPGLL 78

QY 57 W---TCLGSLIISLAVFLMF-----LKRISSEPLKDEPKNTSGSLGNANIDLEKS 107
 Db 79 FGAPALLGLAVLALVGLVSWRRQRRLRGASSSEADGKDAPEPL----- 127

QY 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSDHCFLPAMEGATILVTTK 160
 Db 128 ---DKYII---LSPGISDATAPAMPPEPPTTP---GASVPATLSTELVTTK 177

QY 161 T 161
 Db 178 T 178

RESULT 6
 ID PROM MOUSE STANDARD; PRT; 867 AA.

AC 054930; 035408;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prominin precursor (Antigen Act13 homolog).

OS PROM.
 GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RA Murgilla S., Godfrey W., Buck D.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;

RX MEDLINE=98024147; PubMed=9356465;
 RA Weigmann A., Corbell D., Hellwig A., Hutter W.B.;

RT "Prominin, a novel microvilli-specific polytopic membrane protein of
 RT the apical surface of epithelial cells, is targeted to plasmalemma
 RT protrusions of non-epithelial cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430 (1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED ON THE APICAL SIDE OF
 CC GUT AND URETER BUDS. IN THE ADULT, EXPRESSED AT THE APICAL SIDE
 CC OF THE KIDNEY TUBULES AND OF THE EPENDYMAL LAYER OF THE BRAIN. NOT
 CC EXPRESSED IN GUT, LIVER, LUNG, PITUITARY, ADRENAL, HEART OR
 CC SPLEEN.

CC -1- SIMILARITY: BELONGS TO THE PROMININ FAMILY.
 CC

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF039663; AAB86916.1; -
 CC DR EMBL; AF026269; AAB86715.1; -
 DR MGD; MGI:1100886; Prom.

FT SIGNAL 1 19
 FT CHAIN 20 867
 FT DOMAIN 1 19
 FT TRANSMEM 20 107

FT TRANSMEM 108 128
 FT DOMAIN 129 158
 FT TRANSMEM 159 179

FT DOMAIN 180 434
 FT TRANSMEM 435 455
 FT DOMAIN 456 487

FT TRANSMEM 488 508
 FT DOMAIN 509 794
 FT TRANSMEM 795 815

FT DOMAIN 816 867
 FT TRANSMEM 867 931
 FT CARBOHYD 293 293

FT CARBOHYD 291 291
 FT CARBOHYD 332 332
 FT CARBOHYD 374 374

FT CARBOHYD 415 415
 FT CARBOHYD 554 554
 FT CARBOHYD 581 581

FT CARBOHYD 732 732
 FT CARBOHYD 732 732
 FT CARBOHYD 732 732

FT CARBOHYD 732 732
 FT CARBOHYD 732 732
 FT CARBOHYD 732 732

FT CARBOHYD 732 732
 FT CARBOHYD 732 732
 FT CARBOHYD 732 732

FT CARBOHYD 732 732
 FT CARBOHYD 732 732
 FT CARBOHYD 732 732

FT CONFLICT 844 844 G -> D (IN REF. 2).
 SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
 Query Match 9.0%; Score 86.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACICQRCSSNTPLTCORCYCNASVYNSVGTNAIWMTCGLSLTSLAVFVLMFL 77
 DB 126 LVGCFECMRC-----CNK-CGSEMQROKQNPCKRCGLSLVLCILMSGIIT 176
 QY 78 RKISSEPLDEFPNNGSGLLGMANIDLEKRTGD-EIIL--PRGLRYVEECTCE---- 129
 DB 177 GFVANGQOTRIKGTOK-----LAKSNFRDPQTLLETPEKQIDYVEGYTNTKNA 227
 QY 130 ----DCIKS-----KPKYDSHCFFPLPMEGATILVTK-TNDYCKSLPAL-- 172
 DB 228 FSDLDGIGVGLGRIGKIDQKPKV-----TPVLEETIKAWATAIKQTKALQWSSSLKS 280

173 ---SATEIEKSISA 183
 281 LODMATQTMNLS 294

RESULT 7
 ID FAK2 MOUSE STANDARD; PRT; 1009 AA.
 AC Q9OV59;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
 adhesion focal tyrosine kinase).
 GN PTK2B OR FAK2 OR FYK2 OR RAFTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxId=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Oca S., Hiresowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.,
 RT Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (FAFTK) from megakaryocytes and brain.";
 J. Biol. Chem. 270:27742-27751(1995).
 [2]
 PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RP FAK2 RAT
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Matchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RT Wilm M., Anderregg R.J., Graves L.M., Eary H.S.;
 RT Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 J. Biol. Chem. 271:29993-29998(1996).

CC by FAK activation. Recruitment by Nephrocystin to cell matrix
 CC adhesion initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (by similarity).
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 CC HSP; P08631; IAD5.
 DR MGD; MG1:104908; Ptk2b.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR005189; Focal AT.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF03623; Focal AT; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; phosphorylation.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 701 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 SQ SEQUENCE 1009 AA; 115821 MW; 963959F560F9605 CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLRYVEECTCEDCIKPKRV 138
 DB 249 KFEPT---LAGFANIDQETRYCELIQGNITVDLVIGKIGRLTSQTKRTCLAEFKQI 305
 QY 139 DSDHCFPPAME-----EGATIIIVTKTND-----YCK 166
 DB 306 RSIRCLPHEQTAVVQLGEGAPQSLXIKTSLAEAWMDLIDGYCR 353

RESULT 8
 ID FAK2 RAT STANDARD; PRT; 1009 AA.
 AC P70600; O63201; O88489;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN PTK2B OR FAK2 OR PYK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxId=10116;
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Matchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RT Wilm M., Anderregg R.J., Graves L.M., Eary H.S.;
 RT Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 J. Biol. Chem. 271:29993-29998(1996).

[2] SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=95403356; PubMed=7673154;
RA Sasaki H., Nagura K., Ishino M., Tobioke H., Kotani K., Sasaki T.;
RT "Cloning and characterization of cell adhesion kinase beta, a novel
RL protein-tyrosine kinase of the focal adhesion kinase subfamily.";
J. Biol. Chem. 270:21206-21219(1995).
[3] SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
RP DOMAIN.
RX TISSUE=Hippocampus;
MEDLINE=98311659; PubMed=9645946;
RA Xiong W.-C., Macklem M., Parsons J.T.;
RT "Expression and characterization of splice variants of PYK2, a focal
RL adhesion kinase-related protein.";
J. Cell Sci. 111:1991-1991(1998).
-1- FUNCTION: Involved in calcium induced regulation of ion channel
and activation of the map kinase signaling pathway. May represent
an important signaling intermediate between neuropeptide activated
receptors or neurotransmitters that increase calcium flux and the
downstream signals that regulate neuronal activity. Interacts with
the Sh2 domain of Grb2. May phosphorylate the voltage-gated
potassium channel protein Kv1.2. Its activation is highly
correlated with the stimulation of c-Jun N-terminal kinase
activity.
-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-1- SUBUNIT: Isoform 1, but not isoform 2, interacts with Crk-
associated substrate (Cas), Nephrocystin and GTPase regulator
associated with FAK (Gral).
-1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
induces the membrane-association of the kinase (by similarity).
Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
-1- ALTERNATIVE PRODUCTS: 3 isoforms: 1 (shown here), 2/PRNK and
3/USUS SPECIFICITY: Isoform 1 is expressed at high levels in the
brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
in the spleen and other tissues, whereas isoforms 2 and 3 are
expressed in the spleen and brain (highest in cerebellum).
-1- PTM: Phosphorylated on tyrosines in response to various stimuli
that elevate the intracellular calcium concentration, as well as
by PKC activation. Recruitment by Nephrocystin to cell matrix
adhesions initiates Tyr-402 phosphorylation (by similarity). In
monocytes, adherence to substrata is required for tyrosine
phosphorylation and kinase activation. Angiotensin II,
thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
autophosphorylation and increase kinase activity.
-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
SUBFAMILY.

DR	PROSITE PSS0011; PROTEIN KINASE DOM; 1.
KM	Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
KW	Alternative splicing.
FT	DOMAIN 425 683
FT	NP BIND 431 439
FT	BUILDING 457 457
FT	ACT SITE 549 549
FT	DOMAIN 701 767
FT	DOMAIN 831 869
FT	DOMAIN 868 1009
FT	MOD_RES 402 402
FT	MOD_RES 579 579
FT	VARSPLIC 1 771
FT	VARSPLIC 772 780
FT	VARSPLIC 739 780
FT	CONFLICT 205 205
FT	CONFLICT 807 807
SQ	SEQUENCE 1009 AA; 115784 MW; D435A475BCA49B8 CRC64;
OY	Query Match 8.5%; Score 82; DB 1; Length 1009;
Db	Best Local Similarity 26.9%; Pred. No. 6;
	Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4
OY	88 EFKNSTSGLLGMANIDLESR-----TGDRIIPRGLEYVEECEDCIKSPKV 138
Db	249 KFENT---LAGFANIIDEFYRCCELLQGNNITVDVIGRGIROLTSODTKPTCLAEFKI 305
OY	139 DSDFCEPLPAME-----EGATITVTTRKD-----YCK 166
Db	306 RSIKRLPLERTAVNVLQGLEGAPSLISIKTSSLAEMAMDLIDGYCR 353
RESULT 9	
ID	FAK2_HUMAN STANDARD; PRT; 1009 AA.
AC	Q14289; Q142709; Q134475; Q14290;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (PADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related adhesion focal tyrosine kinase).
GN	PTK2B OR FAK2 OR PYK2 OR RAFTK.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE=Brain;
RX	MEDLINE=95379967; PubMed=7544443;
RA	Liev S., Moreno H., Martinez R., Knoll P., Pelas E., Musacchio J.M., Plowman G.D., Rudy B., Schlessinger J.;
RT	"Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion channel and MAP kinase functions.";
RL	Nature 376:737-745(1995).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE=Hipocampus;
RX	MEDLINE=96453932; PubMed=8838818;
RA	Hezoz H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
RT	"Molecular cloning and assignment of FAK2, a novel human focal adhesion kinase, to pbl1.2-p22 by nonisotopic in situ hybridization.";
RL	Genomics 32:484-486(1996).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE=Hipocampus;
RX	MEDLINE=95403356; PubMed=7673154;
RA	Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.;
RT	"Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrosine kinase of the focal adhesion kinase subfamily.";
RL	J. Biol. Chem. 270:21206-21219(1995).

RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96070905; Pubmed=7499242;
 RA Avraham S., London R., Fu Y., Oca S., Hingorani D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.,
 RT "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Monocytes;
 RX MEDLINE=98211954; Pubmed=9545257;
 RA Li X., Hunter D., Morris J., Haackl J.S., Earp H.S.;
 RT "A calcium-dependent tyrosine kinase splice variant in human
 RT monocytes. Activation by a two-stage process involving adherence and a
 RT subsequent intracellular signal";
 RL J. Biol. Chem. 273:9361-9364(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
 RX Menzel U., Schilhabel M.B., Wen G., Taudien S., Rosenthal A.;
 Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
 RP WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; Pubmed=11493697;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neurotrophic activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas).
 CC Nephrocystin and Grapase regulator associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Most abundant in the brain, with highest
 CC levels in amygdala and hippocampus. Low levels in kidney. Also
 CC expressed in spleen and lymphocytes.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 CC that elevate the intracellular calcium concentration, as well as
 CC by PKC activation. Recruitment by Nephrocystin to cell matrix
 CC adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrate is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U33284; AAC50203.1; -;
 CC EMBL; L49207; AAB47217.1; -;
 CC EMBL; D45853; BAA08289.1; -;
 CC EMBL; U43522; AAC05330.1; -;
 CC DR

DR EMBL; S80542; AAB35701.1; -;
 DR EMBL; AF31103; -; NOT_ANNOTATED_CDS.
 DR HSSP; P86631; IAD5.
 DR Genew; HGNC:9612; PTK2B.
 DR MIM; 601212; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR005189; Focal_AT.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF03623; Focal_AT; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
 KW Alternative splicing.
 KM DOMAIN 425 693
 FT NP BIND 431 439 ATP (BY SIMILARITY).
 FT BINDING 457 457 ATP (BY SIMILARITY).
 FT ACT SITE 549 549 BY SIMILARITY.
 FT DOMAIN 702 767 PRO-RICH.
 FT DOMAIN 831 869 PRO-RICH.
 FT DOMAIN 868 1009 FOCAL ADHESION TARGETING (FAT).
 FT MOD RES 402 402 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD RES 579 579 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT VARSPIC 739 780 MISSING (IN ISOFORM 2).
 FT MUTAGEN 859 859 P->A. LOSS OF INTERACTION WITH
 FT NEPHROCYSTIN.
 FT CONFLICT 23 23 A->G (IN REF. 3).
 FT CONFLICT 256 256 G->P (IN REF. 2).
 FT CONFLICT 435 435 F->L (IN REF. 3).
 FT CONFLICT 780 780 R->G (IN REF. 2).
 SQ SEQUENCE 1009 AA; 115874 MW; 420B21046274E7C2 CRC64;
 Query Match 8.2%; Score 79.5; DB 1; Length 1009;
 Best Local Similarity 32.1%; Pred. No. 10;
 Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;
 QY 88 EFKATGSGILGMANIDLEKSR-----TGDEILIRGLGYEYECTCEDCIKSKRV 138
 DB 249 KEFNT---LAGPANIIDOSTYRELLIGMNITVDVIGKGIROLTSQAKPTCLAEFKOI 305
 QY 139 DSDHCFPLPAMEGATIL 156
 DB 306 RRIKRLPL---REGQAVL 320
 RESULT 10
 T13X HUMAN
 ID T13X HUMAN STANDARD; PRT; 293 AA.
 AC 014836;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; Pubmed=9311921;
 RA von Buehlow G.-U., Bzom R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

RESULT 13
YCSB_SCHPO STANDARD: PRT; 638 AA.
AC 074910;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Hypothetical WD-repeat protein C613.12c in chromosome III.
GN SPC613.12c.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Frazer A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones B., Jones M., Leacher S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares K., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodwards J., Vilella A., Vilella R., Vilella S., Vilella T., Whitehead S.,
RA Wellens I., Venter E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer H., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandt R., Farnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
RA Gaillet F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Pechankin J.,
RA Shpakovski G.V., Useery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
CC
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CC
CC EMBL; AL031644; CAA21064.1; -
CC InterPro; IPR001680; WD40.
CC Pfam; PF00400; WD40. 4.
CC PRINTS; PR00320; GPROTEINRPT.
CC SMART; SM00320; WD40; 4.
CC PROSITE; PS00678; WD_REPEATS_1; 2.
CC PROSITE; PS50082; WD_REPEATS_2; 2.
CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein Repeat; WD repeat.
FT REPEAT 287 336 WD 1.
FT REPEAT 486 525 WD 2.
FT REPEAT 544 583 WD 3.
FT REPEAT 587 626 WD 4.
SQ SEQUENCE 638 AA; 71536 MW; 6CD360D8748AAF98 CRC64;

Query Match 7.8%; Score 75.5; DB 1; Length 638;
Best Local Similarity 22.7%; Pred. No. 15;
Matches 44; Conservative 20; Mismatches 61; Indels 69; Gaps 7;

QY 12 EYFDLHACIPCOLRCSSNTPPLTCQRYCNASVTSYKGNALIMTCLSLISLAVF 71
DB 42 EYDFPYRAELPCP-----KPSLSISKHSAKVSNVNR-----LEQLLTLSTGF 88
QY 72 VLMFLAKISSEPLKDFKRTGSLGMANIDLEKSRGDEILPRGLTYEEC----- 126
DB 89 L-----PNSRPYLSERVRKRTHL-----LSNSINGDDKPSLIHVDFTPEECFIQE 134
QY 127 -----TCDICIKSRKVDSDHCFPLPAMEGATILVT 158
DB 135 AKLAKFPVNSVQFNDAYSTHSPKLGRAYEDC-----QKFIDNPSLSVVDHGAIIIRT 190
QY 159 TKTN-----DYCKS 167
DB 191 YKNNKKLLPDYLS 204
RESULT 14
SRK6_BRAOL STANDARD: PRT; 849 AA.
AC 009052;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE (S-receptor kinase) (SRK).
GN SRK6.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. S656; TISSUE=Stigma;
RX MEDLINE=92020942; PubMed=1681543;
RA Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RT "Molecular cloning of a putative receptor protein kinase gene encoded
RT at the self-incompatibility locus of Brassica oleracea";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
CC -1- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-
CC FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-
CC SPECIFIC GLYCOPROTEINS. INTERACTION WITH A LIGAND IN THE
CC EXTRACELLULAR DOMAIN TRIGGERS THE PROTEIN KINASE ACTIVITY OF THE
CC CYTOPLASMIC DOMAIN.
CC
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER.
CC -1- POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
CC B.OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
CC -1- SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
CC GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
CC A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
CC
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CC
CC EMBL; M76647; AAA33000.1; ALT_TERM.
CC InterPro; IPR001480; B_lectin.
CC InterPro; IPR000719; Euk_kinase.
CC InterPro; IPR003609; Pan_app.
CC InterPro; IPR004040; STY_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR000588; Slocus_glycop.
CC Pfam; PF00069; Kinase; 1.
CC Pfam; PF00954; S_locus_glycop; 1.
CC Pfam; PF01453; Agglutinin; 1.

DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; P4M AP; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; Signal; ATP-binding;
KW Transmembrane; Receptor; Glycoprotein; Self-incompatibility.
FT SIGNAL 1 32
FT CHAIN 33 849
FT FT
FT DOMAIN 33 446
FT TRANSMEM 447 466
FT DOMAIN 467 849
FT DOMAIN 528 779
FT NP_BIND 534 542
FT BINDING 556 556
FT ACT_SITE 653 653
FT CARBOHYD 47 47
FT CARBOHYD 120 120
FT CARBOHYD 196 196
FT CARBOHYD 260 260
FT CARBOHYD 314 314
FT CARBOHYD 389 389
FT CARBOHYD 442 442
SQ SEQUENCE 849 AA; 97231 MW; 7E156059EDDF4370 CRC64;

Query Match 7.8%; Score 75; DB 1; Length 849;
Best Local Similarity 17.6%; Pred. No. 23;
Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

QY 24 COLRGSSNTPPLTCQRYCNASVNSVKGTAIIMT----- 58
DB 380 CKKRCISD---CNCCTFANADIRNG--GSGCVTWTERLEDIRNYATDAIDGQDLYRLAA 434
QY 59 -----CLGLSLIISLAVFLMLRKISSEPLDEPKNTGSGLLGMANIDLEK 106
DB 435 ADIAKKRNASKGISLTGVSALLIMFCL-----WKRQKRAKASISANTQRNQ 487
QY 107 SRTGDEIILPRGLEVEVEECTCEDCKSRKVDSDHCF-----PLPAMEGATILVTKYT 161
DB 488 NLPNMNEMVL-----SSKREFSGEYKFELDELPIEME---TVVAKTEN 527
QY 162 NDYCKSL 168
DB 528 FSSCNKGL 534

QY 15
DB 15
ID ERD1_KLULA STANDARD; PRT; 384 AA.
AC P41771;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ERD1 protein.
GN ERD1.
OS Kluyveromyces lactic (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95084639; PubMed=7992512;
RA Dean N.;
RT "Cloning and DNA sequence of a Kluyveromyces lactic ERD1 homologue.";
RT Year: 10:1117-1124(1994).
CC -!- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC
CC RETICULUM PROTEINS, AFFECTS GLYCOPROTEIN PROCESSING IN THE
CC GOLGI APPARATUS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----

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CC -----
DR EMBL; U04714; AAA21530.1; -
DR InterPro; IPR004342; EXS_Cterm.
DR Pfam; PF03124; EXS; 1.
KW Endoplasmic reticulum; Transmembrane; Protein transport.
FT TRANSMEM 19 36
FT TRANSMEM 78 94
FT TRANSMEM 102 123
SQ SEQUENCE 384 AA; 45315 MW; C064F9A67C96B458 CRC64;

Query Match 7.7%; Score 74.5; DB 1; Length 384;
Best Local Similarity 27.2%; Pred. No. 11;
Matches 43; Conservative 21; Mismatches 55; Indels 39; Gaps 8;

QY 9 SONEYPDSILNACIPCOLRGSSNTPPLTCQRYCNASVNSVKGTAIIMTCLGLSLISL 68
DB 67 SSKLKFSSISRYIIPWOLVC-----IILFOY---SFTNNV--SNKLLMFPLNLSPLLEL 115
QY 69 AVFVLMFLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRGDEIILPRGLEVEVEECTC 128
DB 116 -FYIFAMILR--SSAMVARCPRG---ILWVADIEPKRYNNYIISDTLSY----- 161
QY 129 EDCIKSRKPKVSDHCFPLPAMEGATILVTKTNDYCK 166
DB 162 -----SKPLVD-----LAIYATFLFHDPTNVKQC 185

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